



#4

SEQUENCE LISTING

<110> Cockett, Mark I.

Cilks, Daniel W.

Chang Ling, Huai-Ping

Sokol, Patricia T.

<120> Human Potassium Channel Polynucleotides and
Polypeptides and Uses Therefor

<130> AHP 98089 D1

<140> 10/062,879

<141> 2002-01-31

<160> 4

<170> PatentIn Ver. 2.0

<210> 1

<211> 2121

<212> DNA

<213> human

<400> 1

gatttgcgtga actaactcca agctgggtgtg cctagcgtcc ggcggcgtgc cggcccaaga 60
gctggagtca ccatggcgcc cgaggttgcg .gcctggctgc cttttgcggcc 120
atcgggtgga tgccgggtggc caactgcccc atgcccctgg ccccgccga caagaacaag 180
cggcaggatg agctgattgt cctcaacgtg agtggcgga gttccagac ctggaggacc 240
acgctggagc gctaccccgga caccctgtcg ggcagcacgg agaaggagtt cttcttcaac 300
gaggacacca aggagtactt cttcgaccgg gaccccgagg tggccgtcg cgtctcaac 360
ttctaccgca cggggaaagct gcaactacccg cgctacgagt gcatctctgc ctacgacgac 420
gagctggcct tctacggcat cttccggag atcatgggg actgctgcta cgaggagta 480
aaggaccgca agagggagaa cgccgagcgg ctcatggacg acaacgactc ggagaacaac 540
caggagtcca tgccctcgct cagttccgc cagaccatgt ggcgggcctt cgagaacccc 600
cacaccagca cgtggccct ggtttctac tacgtgactg gcttettcat cgctgtctcg 660
gtcatcacca acgtgggtgg aacgggtgccc tgccgcacgg tcccggcag caaggagctg 720
ccgtgggggg agcgtactc ggtggccctt ttctgcctgg acacggcgtg cgtcatgatc 780
ttcacccgtgg agtacctctt cggcgtcttc cggcgtccca gccgctaccc cttcatccgc 840
agcgtcatga gcatcatcga cgtggggcc atcatggcc actacatcg tctggtcatg 900
accaacaacg aggacgtgtc cggcgccttc gtcacgctcc gggtcttccg cgtttcagg 960
atcttcaagt ttccccgcca ctccccagggc ctggcgatcc tgggctacac actgaagagc 1020
tgtgcctcc aacggggctt tcttccttc tccctcacca tggccatcat cattttgc 1080
actgtgtatgt tttatgcccga gaagggctcc tggccagca agttcacaag catccctgccc 1140
tcgttttgtt acaccattgt caccatgaccc acactggat acggagacat ggtgcctaag 1200
acgatttgcag ggaagatctt cggcgtccatc tgcgcgttga gtggcgctcc ggtcattgcc 1260
ctgcccgtcc ctgtgtattgt ttccaaacttt agccggatcc accaccagaa tcagagagct 1320
gataaaacgca gggcacaaaaa gaaaggcccgc cttgcccagga tccgtgtggc caaaacaggc 1380

RECEIVED
MAR 22 2002
TECH CENTER 1600/2900

agttcgaatg catacctgca cagcaagcgc aacgggctcc tcaacgaggc gctggagctg 1440
acgggcaccc cagaagagga gcacatggc aagaccacct cactcatcga gagccagcat 1500
catcacctgc tgcaactgcct ggaaaaaacc actgggttgc cctatcttgc ggtatgtccc 1560
ctgttatctg taccaacacctc caccatcaag aaccacgagt ttatgtatga gcagatgttt 1620
gagcagaact gcattggagag ttcaatgcag aactacccat ccaaaagaag tccctcactg 1680
tccagccacc caggcctcac taccacctgc tgctcccgtc gtagtaagaa gaccacacac 1740
ctgcccattt ctaacctgcc agctactcgc ctgcgcagca tgcaagagct cagcacgatc 1800
cacatccagg gcagtggagca gcccctccctc acaaccagtc gctccagcct taatttggaa 1860
gcagacgacg gactggagacc aaactgcaaa acatcccaga tcaaccacagc catcatcagc 1920
atccccactc ccccaagcgtc aaccccaagag gggaaaagtc ggccacccccc tgccagccca 1980
ggccccaaca cgaacattcc ttccataacc agcaatgttg tcaaggtctc tgtttgtaa 2040
aaatcccgcg gccatggcg ggggagcat gcgacgtcg gcccaattcg ccctatagtg 2100
agtgtttaa aagccgaatt c 2121

<210> 2
<211> 655
<212> PRT
<213> human

<400> 2

Met Ala Ala Gly Val Ala Ala Trp Leu Pro Phe Ala Arg Ala Ala Ala
1 5 10 15

Ile Gly Trp Met Pro Val Ala Asn Cys Pro Met Pro Leu Ala Pro Ala
20 25 30

Asp Lys Asn Lys Arg Gln Asp Glu Leu Ile Val Leu Asn Val Ser Gly
35 40 45

Arg Arg Phe Gln Thr Trp Arg Thr Thr Leu Glu Arg Tyr Pro Asp Thr
50 55 60

Leu Leu Gly Ser Thr Glu Lys Glu Phe Phe Asn Glu Asp Thr Lys
65 70 75 80

Glu Tyr Phe Phe Asp Arg Asp Pro Glu Val Phe Arg Cys Val Leu Asn
85 90 95

Phe Tyr Arg Thr Gly Lys Leu His Tyr Pro Arg Tyr Glu Cys Ile Ser
100 105 110

Ala Tyr Asp Asp Glu Leu Ala Phe Tyr Gly Ile Leu Pro Glu Ile Ile
115 120 125

Gly Asp Cys Cys Tyr Glu Glu Tyr Lys Asp Arg Lys Arg Glu Asn Ala
130 135 140

Glu Arg Leu Met Asp Asp Asn Asp Ser Glu Asn Asn Gln Glu Ser Met

145 150 155 160

Pro Ser Leu Ser Phe Arg Gln Thr Met Trp Arg Ala Phe Glu Asn Pro
165 170 175

His Thr Ser Thr Leu Ala Leu Val Phe Tyr Tyr Val Thr Gly Phe Phe
180 185 190

Ile Ala Val Ser Val Ile Thr Asn Val Val Glu Thr Val Pro Cys Gly
195 200 205

Thr Val Pro Gly Ser Lys Glu Leu Pro Cys Gly Glu Arg Tyr Ser Val
210 215 220

Ala Phe Phe Cys Leu Asp Thr Ala Cys Val Met Ile Phe Thr Val Glu
225 230 235 240

Tyr Leu Leu Arg Leu Phe Ala Ala Pro Ser Arg Tyr Arg Phe Ile Arg
245 250 255

Ser Val Met Ser Ile Ile Asp Val Val Ala Ile Met Pro Tyr Tyr Ile
260 265 270

Gly Leu Val Met Thr Asn Asn Glu Asp Val Ser Gly Ala Phe Val Thr
275 280 285

Leu Arg Val Phe Arg Val Phe Arg Ile Phe Lys Phe Ser Arg His Ser
290 295 300

Gln Gly Leu Arg Ile Leu Gly Tyr Thr Leu Lys Ser Cys Ala Ser Glu
305 310 315 320

Leu Gly Phe Leu Leu Phe Ser Leu Thr Met Ala Ile Ile Ile Phe Ala
325 330 335

Thr Val Met Phe Tyr Ala Glu Lys Gly Ser Ser Ala Ser Lys Phe Thr
340 345 350

Ser Ile Pro Ala Ser Phe Trp Tyr Thr Ile Val Thr Met Thr Thr Leu
355 360 365

Gly Tyr Gly Asp Met Val Pro Lys Thr Ile Ala Gly Lys Ile Phe Gly
370 375 380

Ser Ile Cys Ser Leu Ser Gly Val Leu Val Ile Ala Leu Pro Val Pro
385 390 395 400

Val Ile Val Ser Asn Phe Ser Arg Ile Tyr His Gln Asn Gln Arg Ala

405 410 415
Asp Lys Arg Arg Ala Gln Lys Lys Ala Arg Leu Ala Arg Ile Arg Val
420 425 430
Ala Lys Thr Gly Ser Ser Asn Ala Tyr Leu His Ser Lys Arg Asn Gly
435 440 445
Leu Leu Asn Glu Ala Leu Glu Leu Thr Gly Thr Pro Glu Glu Glu His
450 455 460
Met Gly Lys Thr Thr Ser Leu Ile Glu Ser Gln His His His His Leu Leu
465 470 475 480
His Cys Leu Glu Lys Thr Thr Gly Leu Ser Tyr Leu Val Asp Asp Pro
485 490 495
Leu Leu Ser Val Arg Thr Ser Thr Ile Lys Asn His Glu Phe Ile Asp
500 505 510
Glu Gln Met Phe Glu Gln Asn Cys Met Glu Ser Ser Met Gln Asn Tyr
515 520 525
Pro Ser Thr Arg Ser Pro Ser Leu Ser Ser His Pro Gly Leu Thr Thr
530 535 540
Thr Cys Cys Ser Arg Arg Ser Lys Lys Thr Thr His Leu Pro Asn Ser
545 550 555 560
Asn Leu Pro Ala Thr Arg Leu Arg Ser Met Gln Glu Leu Ser Thr Ile
565 570 575
His Ile Gln Gly Ser Glu Gln Pro Ser Leu Thr Thr Ser Arg Ser Ser
580 585 590
Leu Asn Leu Lys Ala Asp Asp Gly Leu Arg Pro Asn Cys Lys Thr Ser
595 600 605
Gln Ile Thr Thr Ala Ile Ile Ser Ile Pro Thr Pro Pro Ala Leu Thr
610 615 620
Pro Glu Gly Glu Ser Arg Pro Pro Pro Ala Ser Pro Gly Pro Asn Thr
625 630 635 640
Asn Ile Pro Ser Ile Thr Ser Asn Val Val Lys Val Ser Val Leu
645 650 655

<210> 3
<211> 2064
<212> DNA
<213> human

<400> 3

gatttgcgtga actaactcca agctgggtgtc cctagcgtcc gcgcggctgc cggcccaaga 60
gctggagtca ccatacgccgc cggagttgcg gcctggctgc cttttgcgg 99ctgcggcc 120
atcgggtggta tgccgggtggc caactgcccc atgccccctgg ccccgccga caagaacaag 180
cggcaggatg agctgattgt cctcaacgtg agtggggcgg a gttccagac ctggaggacc 240
acgctggagc gctaccccgga caccctgtg ggcacgacgg agaaggagtt cttttcaac 300
gaggacacca agaggtactt ctgcacccgg gaccccgagg tggccgtg cgtctcaac 360
ttctaccgca cggggaaact gcaactacccg cgctacgagt gcatctctgc ctacgacgac 420
gagctggct tctacggcat cttccggag atcatgggg actgctgta cgaggagttac 480
aaggaccgca agagggagaa cggccgacgg ctcatggacg acaacgactc ggagaacaac 540
caggagtccs tggccctcgct cagttccgc cagaccatgt ggcgggcctt cgagaacccc 600
cacaccagca cgctggccct ggtcttctac tacgtgactg gcttcttcat cgctgtctcg 660
gtcatcacca acgtgggtggaa gacgggtggc tgccggcacgg tcccgccag caaggagctg 720
ccgtgcgggg agcgctactc ggtggccctt ttctgcctgg acacggcgtg cgtcatgatc 780
ttcacccgtgg agtacccctt ggggtcttc ycgctccca gccgctaccg cttcatccgc 840
agcgtcatga gcatcatcga cgtgggtggcc atcatggccct actacatcgg tctggcatg 900
accaacaacg aggacgtgtc cggcgccctt gtcacgctcc gggcttccg cgtcttcagg 960
atcttcaagt ttcccgccca ctccccaggcc ctgcggatcc tgggctacac actgaagagc 1020
tggccctccg aactgggctt ttttcttc tccctccca tggccatcat catcttgcc 1080
actgtgatgt ttatgccga gaagggtctcc tcgcccagca agttcacaag catccctgcc 1140
tcgttttgtt acaccattgtt caccatgacc acactggat acggagacat ggtgcctaag 1200
acgatttgcag ggaagatctt cggctccatc tgccttgc gttggcgtcc ggtcattgcc 1260
ctgccagtcc ctgtgattgt ttccaaactt agccggattt accaccagaa tcagagagct 1320
gataaacgca gggcacaaaaa gaaggcccgc ctgccagga tccgtgtggc caaaacaggc 1380
agttcgaatg catacctgca cagcaagcgc aacgggctcc tcaacgaggc gctggagctg 1440
acgggcaccc cagaagagga gcacatgggc aagaccaccc cactcatcga gagccagcat 1500
catcacccgca tgcactgcct ggaaaaacc actaaccacg agtttattga tgagcagatg 1560
tttgagcaga actgcatttgc gatgtcaatg cagaactacc catccacaag aagtccctca 1620
ctgtccaccc acccaggccct cactaccacc tgcgtctccc gtcgttagtaa gaagaccaca 1680
cacctgccccca attctaacct gccagctact cgcctgcgc gcatgcaaga gctcagcaccg 1740
atccacatcc agggcagtga gcaagccctcc ctccacaacca gtcgcctccag ctttaatttg 1800
aaagcagacg acggactgag accaaactgc aaaacatccc agatcaccac agccatcatc 1860
agcatccccca ctccccccagc gctaacccca gaggggaaa gtcggccacc ccctgccaqc 1920
ccaggccccca acacgaacat tccctccata accagcaatg ttgtcaaggt ctctgtcttg 1980
taaaaatccc gggccatgg cggccggag catgcacgt cggcccaat tcgcccata 2040
gtgagtcgttaaaagccga attc 2064

<210> 4
<211> 636
<212> PRT
<213> human

<400> 4

Met Ala Ala Gly Val Ala Ala Trp Leu Pro Phe Ala Arg Ala Ala Ala
1 5 10 15

Ile Gly Trp Met Pro Val Ala Asn Cys Pro Met Pro Leu Ala Pro Ala
20 25 30

Asp Lys Asn Lys Arg Gln Asp Glu Leu Ile Val Leu Asn Val Ser Gly
35 40 45

Arg Arg Phe Gln Thr Trp Arg Thr Thr Leu Glu Arg Tyr Pro Asp Thr
50 55 60

Leu Leu Gly Ser Thr Glu Lys Glu Phe Phe Asn Glu Asp Thr Lys
65 70 75 80

Glu Tyr Phe Phe Asp Arg Asp Pro Glu Val Phe Arg Cys Val Leu Asn
85 90 95

Phe Tyr Arg Thr Gly Lys Leu His Tyr Pro Arg Tyr Glu Cys Ile Ser
100 105 110

Ala Tyr Asp Asp Glu Leu Ala Phe Tyr Gly Ile Leu Pro Glu Ile Ile
115 120 125

Gly Asp Cys Cys Tyr Glu Glu Tyr Lys Asp Arg Lys Arg Glu Asn Ala
130 135 140

Glu Arg Leu Met Asp Asp Asn Asp Ser Glu Asn Asn Gln Glu Ser Met
145 150 155 160

Pro Ser Leu Ser Phe Arg Gln Thr Met Trp Arg Ala Phe Glu Asn Pro
165 170 175

His Thr Ser Thr Leu Ala Leu Val Phe Tyr Tyr Val Thr Gly Phe Phe
180 185 190

Ile Ala Val Ser Val Ile Thr Asn Val Val Glu Thr Val Pro Cys Gly
195 200 205

Thr Val Pro Gly Ser Lys Glu Leu Pro Cys Gly Glu Arg Tyr Ser Val
210 215 220

Ala Phe Phe Cys Leu Asp Thr Ala Cys Val Met Ile Phe Thr Val Glu
225 230 235 240

Tyr Leu Leu Arg Leu Phe Ala Ala Pro Ser Arg Tyr Arg Phe Ile Arg
245 250 255

Ser Val Met Ser Ile Ile Asp Val Val Ala Ile Met Pro Tyr Tyr Ile
260 265 270

Gly Leu Val Met Thr Asn Asn Glu Asp Val Ser Gly Ala Phe Val Thr
275 280 285

Leu Arg Val Phe Arg Val Phe Arg Ile Phe Lys Phe Ser Arg His Ser
290 295 300

Gln Gly Leu Arg Ile Leu Gly Tyr Thr Leu Lys Ser Cys Ala Ser Glu
305 310 315 320

Leu Gly Phe Leu Leu Phe Ser Leu Thr Met Ala Ile Ile Ile Phe Ala
325 330 335

Thr Val Met Phe Tyr Ala Glu Lys Gly Ser Ser Ala Ser Lys Phe Thr
340 345 350

Ser Ile Pro Ala Ser Phe Trp Tyr Thr Ile Val Thr Met Thr Thr Leu
355 360 365

Gly Tyr Gly Asp Met Val Pro Lys Thr Ile Ala Gly Lys Ile Phe Gly
370 375 380

Ser Ile Cys Ser Leu Ser Gly Val Leu Val Ile Ala Leu Pro Val Pro
385 390 395 400

Val Ile Val Ser Asn Phe Ser Arg Ile Tyr His Gln Asn Gln Arg Ala
405 410 415

Asp Lys Arg Arg Ala Gln Lys Lys Ala Arg Leu Ala Arg Ile Arg Val
420 425 430

Ala Lys Thr Gly Ser Ser Asn Ala Tyr Leu His Ser Lys Arg Asn Gly
435 440 445

Leu Leu Asn Glu Ala Leu Glu Leu Thr Gly Thr Pro Glu Glu Glu His
450 455 460

Met Gly Lys Thr Thr Ser Leu Ile Glu Ser Gln His His His Leu Leu
465 470 475 480

His Cys Leu Glu Lys Thr Thr Asn His Glu Phe Ile Asp Glu Gln Met
485 490 495

Phe Glu Gln Asn Cys Met Glu Ser Ser Met Gln Asn Tyr Pro Ser Thr
500 505 510

Arg Ser Pro Ser Leu Ser Ser His Pro Gly Leu Thr Thr Thr Cys Cys
515 520 525

Ser Arg Arg Ser Lys Lys Thr Thr His Leu Pro Asn Ser Asn Leu Pro
530 535 540

Ala Thr Arg Leu Arg Ser Met Gln Glu Leu Ser Thr Ile His Ile Gln
545 550 555 560

Gly Ser Glu Gln Pro Ser Leu Thr Thr Ser Arg Ser Ser Leu Asn Leu
565 570 575

Lys Ala Asp Asp Gly Leu Arg Pro Asn Cys Lys Thr Ser Gln Ile Thr
580 585 590

Thr Ala Ile Ile Ser Ile Pro Thr Pro Pro Ala Leu Thr Pro Glu Gly
595 600 605

Glu Ser Arg Pro Pro Pro Ala Ser Pro Gly Pro Asn Thr Asn Ile Pro
610 615 620

Ser Ile Thr Ser Asn Val Val Lys Val Ser Val Leu
625 630 635